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EVOLVING VIEWS ON ENTERIC VIRAL INFECTIONS OF EQUINES: AN APPRAISAL OF KEY PATHOGENS

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ABSTRACT

Equines, the earliest known mammalian species, have been found highly susceptible to several enteric pathogens including viruses, fungi, parasites and bacteria. This review conserves with the key viral pathogens that affects foals and horses such as rotavirus, adenovirus, coronavirus, parvovirus, picobirnavirus etc. With the advent of next generation sequencing approaches the list of new enteric viruses has expanded. Viruses like Cyclovirus, Kirkovirus and Anellovirus are the new members identified in equines recently. Close proximity of horses to human settlements and/or other domestic animals pretense the threat of infectious diseases spread to humans/animals and vice-versa. Therefore, horse diseases are not only of veterinary importance but also are among important factors for public health. Herein, we intend to appraise current status of key enteric viruses that cause diarrheic disorders in foals and horses.

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1 Introduction

Equines are among the earliest known mammalian species that have been incessantly domesticated by the human race since 4000 BC. Apart from being companion animals to humans, they have also been used as amusing or sporting animal. During late 19th century, equine microbiology came under existence with the discovery of *Burkholderia mallei* as the feared pathogen of glanders and farcy of horse. Later on, a filterable agent was identified capable of causing African horse sickness (Slater, 2013). With the help of classic virological methods, numerous equine viruses have been added to this list such as equine influenza virus, West Nile virus, equid herpesviruses, equine encephalitis viruses, equine arteritis virus, equine infectious anemia virus, equine coronavirus, Hendra virus and vesicular stomatitis virus. Though, the study of equine infectious diseases has been an important part of veterinary sciences since ages, a large number of the equine diseases still remains unfamiliar. Close proximity of horses to human settlements and to other domestic animals pose the threat of infectious diseases spread to humans/animals and vice-versa. Zoonotic pathogens such as Alphaviruses, Hendra virus, Influenza A virus, Rabies virus and West Nile virus are reported to infect horses (Johnson, 2011; Cullinane & Newton, 2013; Onmaz et al., 2013; Slater, 2013). It is therefore noteworthy that horse diseases are not only of veterinary importance but also pose potential threat of zoonosis/reverse zoonosis (Khurana et al., 2015; Mukarim et al., 2015) and are among important factors from human public health perspective.

Several enteric pathogens leading to multifactorial diseases have been detected and isolated from diseased foals and horses. The major enteric pathogens associated with neonatal foal diarrhea are rotavirus, coronavirus, *Clostridium perfringens* type A, *Salmonella* spp., *Rhodococcus equi* and *Clostridium difficile* (Fielding et al., 2015; Franco Ayala & Oliver Espinosa, 2015; Barr, 2016). Foals co-infecting with number of infectious agents has also been documented in diarrheic foals (Slovis et al., 2014). One of the prime causes of equine enteritis is the viral infections. A recent metagenomics study highlighted several new viruses like Cyclovirus, Kirkovirus and Anellovirus along with known enteric viruses such as parvovirus, adenoviruses, coronaviruses, rotaviruses and picobirnaviruses in equines (Li et al., 2015). In last few years, several reviews appeared on various aspects of equine health excluding enteric viral pathogens of equines, except a few that highlighted coronavirus and rotavirus infections in equines (Bailey et al., 2013; Papp et al., 2013; Dhama et al., 2014; Pusterla et al., 2015a). Viral etiological agents which are able to cause diarrheic outbreaks are comprehended in Table 1. In the event of emergence of several new viral infections worldwide including Ebola and Zika (Dhama et al., 2015a; Singh et al., 2016) there is urgent need to understand the burden of viral infections in different animal hosts. Here, we intend to review current status of major enteric viruses of

economic importance that cause diarrheic disorders in foals and horses. Furthermore, current updates in the rotavirus and coronavirus infection in equines are covered.

2 Adenovirus

Adenoviruses belong to the *Adenoviridae* family, are un-enveloped and have icosahedral nucleocapsid, with 90–100 nm size, encapsulating a dsDNA genome of 26–45 Kbp (Davison et al., 2003). Adenoviruses are known to affect a wide vertebrate's host range and are genetically/antigenically heterogeneous (Harrach et al., 2011). Presently, this family comprises of 5 genera as Mastadenovirus, Atadenovirus, Aviadenovirus, Ichtadenovirus and Siadenovirus (Harrach et al., 2011).

Horses and foals are affected by adenoviruses of genera Mastadenovirus, have been primarily connected with respiratory and gastrointestinal tract infections (Reubel & Studdert, 1997; Cavanagh et al., 2012). Equine adenoviruses are separated into 2 serotypes and consequent molecular and phylogenetic readings established them as distinct species which are nowadays called as Equine adenovirus 1 (EAdV-1) and Equine Adenovirus 2 (EAdV-2) (Reubel & Studdert, 1997; Cavanagh et al., 2012). Out of these two, EAdV-1 is primarily associated with infections in the respiratory tract of young foals and horses whereas EAdV-2 has been reported mainly from horses having diarrheal illness (Studdert & Blackney, 1982). The first equine adenovirus was reported and isolated in USA (Todd, 1969) it was followed by isolation reports from Germany and Australia whereas physical characterization of the virus was published in 1973 of an adenovirus isolated from the pneumonic lung tissue of an Arabian foal (Ardans et al., 1973).

Antibodies pertaining to both the Equine Adenovirus types were reported in New South Wales, Australia (Giles et al., 2010). In a study during 1982 on the diarrheal outbreaks in young foals, researchers isolated and identified an Equine adenovirus strain which did not contain the hemagglutination-inhibiting antibody to EAdV-1 (Studdert & Blackney, 1982). Similar research findings were published in New Zealand revealing two serologically different EAdV strains isolated from thoroughbred foals suffering from diarrhea and respiratory disease (Horner & Hunter, 1982). These research findings supported the assumption that adenoviruses found in the fecal specimens should be considered as the prototype for EAdV-2. Compared to EAdV-1 adenovirus there has been less studies done with respect to EAdV-2 adenovirus with the very first sequence data appeared on the GenBank database for EAdV-2 in the year 1997 (Reubel & Studdert, 1997) (GenBank L80007.1). The study by Reubel and Studdert also established the first molecular evidence that EAdV-2 is distinct to EAdV-1, not only in antigenic aspect but is quite different on molecular level too.

Table 1 Enteric viruses reported in equines having relevance in causing enteritis highlighting their main features.

Sl No.	Viruses	Genome	Genus	Species/serotypes	Relevance in enteric diseases	References
1.	Adenoviruses	dsDNA	Mastadenovirus	Equine Adenovirus 1	No	Cavanagh et al.(2012)
				Equine Adenovirus 2	Yes	Giles et al. (2015)
2.	Coronaviruses	ssRNA	Betacoronavirus	Betacoronavirus-1	Yes	Nemoto et al. (2015b)
3.	Rotaviruses	dsRNA	Rotavirus A	G3P[12], G14P[12], G3P[3], G5P[7], G6P[1], G8P[1], G10P[1], G10P[11] and G13P[18]	Yes	Ghosh & Kobayashi (2014)
4.	Picobirnavirus	dsRNA	Picobirnaviruses	Equine picobirnavirus	Yes	Li et al. (2015)
5.	Parvovirus	ssDNA	Copiparvovirus	Ungulate Copiparvovirus 3	No	Li et al. (2015)
6.	Anellovirus	ssDNA	Mutorquevirus	Unclassified	No	Li et al. (2015)
7.	Cyclovirus	ssDNA	Cyclovirus	Unclassified	No	Li et al. (2015)

A whole genome characterization of an EAdV-2 strain was also reported recently in the year 2015 in Australia (Giles et al., 2015) (GenBank Acc. No. KT160425). Interestingly, till this review in September 2016 there were only 2 sequence report available for EAdV-2 in the GenBank database out of which one is complete genome and another is 5.5 kbp in length comprising the hexon and endopeptidase genes.

Unlike EAdV-1, which can be easily isolated and grows fastidiously in primary tissue culture derived from equine fetal kidney (EFK) cells (Studdert, 1978), EAdV-2 responds very poorly to cell culture and has been infrequently isolated (Horner & Hunter, 1982; Studdert & Blackney, 1982). The major technique used for the diagnosis and characterization of adenovirus is PCR which is based on the hexon gene of adenovirus genome which contains highly conserved regions (Reubel & Studdert, 1997).

With the available literature regarding the infection of adenovirus in equines EAdV-1 has been studied widely in comparison to EAdV-2. Despite the significant improvement in the development of diagnostic techniques there has been scarcity of information regarding EAdV-2 which requires the attention of veterinarians and scientist working in the field of equine infectious diseases.

3 Coronavirus

Coronavirus is an enveloped, ssRNA, positive sense virus having a helical symmetry with a genome length of 26 to 32 Kb, which is largest among the RNA viruses. The *Coronaviridae* family is divided into 2 subfamilies (*Torovirinae* and *Coronavirinae*). The later subfamily classified into four different genera viz. Alphacoronavirus, Betacoronavirus, Deltacoronavirus and Gammacoronavirus based on the serological and molecular differences (Woo et al., 2012). These are mainly associated with respiratory, neurologic, hepatic or gastrointestinal disorders in animals

(Holmes, 2001). The different animals reported to have Coronavirus mediated infections are swine, cattle, horse, dog, cat and avian species like chicken and turkey (Saif et al., 1991; White & Fenner, 1994; Studdert, 1996; Jamieson et al., 1998; Guy et al., 2000; Lai & Holmes, 2001; McIntosh, 2002; Strauss & Strauss, 2002; Ksiazek et al., 2003; Van der Hoek et al., 2004; Brian & Baric, 2005; Weiss & Navas-Martin, 2005; Decaro & Buonavoglia, 2008; Boileau & Kapil, 2010; Woo et al., 2012).

Further, based on the antigenic properties coronaviruses are divided into 3 major antigenic groups which infect several animal hosts and humans (group 1 and 2) and also avian species (group 2). The group 1 comprise of human coronavirus (strain 229E), canine coronavirus, porcine transmissible gastroenteritis virus and feline infectious peritonitis virus. The group 2 is represented by human coronavirus strains (OC43 and HKU1), murine hepatitis virus, bovine coronavirus, porcine hemagglutinating encephalomyelitis virus, canine respiratory coronavirus (Erles et al., 2007), and bubaline coronavirus (Decaro et al., 2010). Viruses such as turkey coronavirus and infectious bronchitis virus are included in group 3 (Resta et al., 1985; Studdert, 1996; Davis et al., 2000; Guy et al., 2000; Lai & Holmes, 2001; McIntosh, 2002; Strauss & Strauss, 2002; Van der Hoek et al., 2004; Smith & Denison, 2012; Woo et al., 2012; Smith et al., 2013).

The earliest known *Equine Coronavirus* (ECoV) recognized by electron microscopy (EM) in the foals diarrheic fecal samples and adult horses (Bass & Sharpee, 1975; Huang et al., 1983). Later, in 2000 Davis and colleagues developed an antigen capture ELISA for the detection ECoV in the feces of diarrheic foal along with immunohistochemistry of affected foal's intestine suffering from neonatal enterocolitis (Davis et al., 2000). In the same year, an ECoV strain NC99 was isolated and its N protein gene was characterized using the previously described BCoV primers (Guy et al., 2000). The ECoVs have been found highly related with bovine coronaviruses (Imagawa

et al., 1990; Guy et al., 2000). Subsequently, the complete genomic constellation of ECoV (strain NC99) was achieved which consists of 2 replicase polyproteins, 4 accessory proteins (ns2, p4.7, p12.7, and I) and 5 structural proteins viz. spike, hemagglutinin esterase, membrane, envelope and nucleocapsid (Zhang et al., 2007).

Diagnosis of coronaviruses has been routinely done through EM in the earlier times (Reed et al., 1983; Biermann et al., 1991; Guy et al., 2000). Using BCV antibodies serum neutralization tests has also been employed to detect ECoV infections in horses (Bass & Sharpee, 1975; Imagawa et al., 1990; Anzai et al., 2001). Molecular techniques like nested PCR and quantitative PCR have been actively used in the diagnosis of ECoV (Guy et al., 2000; Slovis et al., 2010). During early stages of infection highly sensitive technique like real-time RT-PCR has been used (Pusterla et al., 2013; Miszczak et al., 2014). In 2015, a RT-LAMP was also developed for the isothermal detection of ECoV which can be economical in comparison to other diagnostic tests (Nemoto et al., 2015a). Recently a one-step real time RT-PCR was also developed and demonstrated for the sensitive detection of ECoV in respiratory and fecal samples (Miszczak et al., 2016). Improving the specificity of the detection one ELISA was recently developed for the specific detection of ECoV in naturally infected horses and record the seroprevalence in them (Kooijman et al., 2016).

In earlier studies, ECoV was suspected to cause enteritis in foals but their pathogenicity in young foals remained unproven (Davis et al., 2000; Van der Hoek et al., 2004; Arguedas, 2007). Mainly the tissue tropism for ECoV infections have been found to be inside the gastrointestinal tract of young foals and horses (Miszczak et al., 2014; Fielding et al. 2015; Pusterla et al., 2015b). Multiple ECoV outbreaks have occurred in the USA and Japan (Oue et al., 2011; Oue et al., 2013; Pusterla et al., 2013). Besides the possible respiratory and mechanical transmission of coronaviruses in equines, infections spreads through fecal-oral route (Studdert, 1996; Anzai et al., 2001). Although, signs of upper respiratory tract infections are predominant with ECoV infected foals but their infrequent detection in nasal secretions shows their lack of tropism to the upper respiratory tract of young horses. In an experimental study on Japanese draught horses, the horses were experimentally inoculated with ECoV strain NC99 and Obihiri 12-2 to confirm and investigate the clinical signs and virus shedding pattern of ECoV in horses.

Though, nasal secretions came positive in PCR assay, experiments could not define whether this was due to nasal replication of the virus and subsequent shedding or due to environmental factors or both (Nemoto et al., 2014). Subsequently, in 2015 a study reported the whole genome sequencing of three earlier isolated ECoV strains from Japan Obihiri 12-1, Obihiri 12-2 and Tokachi09. The study found the three strains genetically similar to NC99 strains of USA with minor exceptions in NS2, NSP3 and p4.7 genes (Nemoto et al., 2015b).

It has been usually observed that ECoV infection in horses spread when they are sheltered together, which has been confirmed by the presence of BCoV and other related coronavirus antibodies in the feces of horses (Imagawa et al., 1990; Anzai et al., 2001). Better management practices regarding the sheltering and transit of young foals and adult horses can arrest the infection from spreading to other places.

4 Rotaviruses

Rotaviruses are the foremost cause of diarrhea in neonates of humans, animals and avian (Estes & Kapikian, 2007; Dhama et al., 2015b). Till date, nine different species have been identified in rotaviruses from (A-I) as per the antigenic differences in the major inner capsid protein and nucleotide sequence identities gene encoding the VP6 protein (Matthijnssens et al., 2012a; Mihalov-Kovacs et al., 2015), although recently reported species I needs further endorsement by the ICTV. Rotaviral genome is made up of eleven dsRNA segments that encode 6 structural proteins viz; VP1, VP2, VP3, VP4, VP6 & VP7 and 5/6 non-structural proteins i.e. NSP1–NSP5/6). The major coat proteins (VP4 & VP7) induce the neutralizing antibodies production and are considered important due to the genetic classification which is based on these genes. As per the latest update of Rotavirus Classification Work Group (RCWG) till 27th June, 2016 there are 32 G-genotypes (VP7) and 47 P-genotypes (VP4) reported in various host species (<https://rega.kuleuven.be/cev/viralmetagenomics/virus-classification/rcwg>).

Among all the species of rotavirus, only group A rotaviruses (RVA) has been detected in the equines so far (Matthijnssens et al., 2012b). The first detection of equine RV has been reported in the year 1975 from England (Flewett et al., 1975). Since from this, equine RVs have been known to be the major causes of diarrhea in foals (Imagawa et al., 1991; Collins et al., 2008; Frederick et al., 2009). Based on the serological reports equine RVAs have been shown to be ubiquitous in the equine populations (Pearson et al., 1982).

Numbers of diagnostic techniques have been employed for detecting RVs in diarrheic foals and adult horses. Electron microscopy was the first technique to be applied for the identification of RVs in foals but unfortunately it requires costly instruments and expertise. Moreover the diagnostic sensitivity of EM turns out to be very low as it can't detect virus particles lower than 10⁷ per ml of stool samples (McIntosh, 1996). Culturing the RV in cell line is again a daunting task. Equine RV has been isolated in MA-104 cell line in the year 1981 when field sample from a diarrheic foal has been successfully adapted in UK (Imagawa et al., 1981). RNA-PAGE has been widely applied for the detection of equine RVs due to the peculiarity of different RV groups to migrate differently on the RNA-PAGE. Certain studies has reported the typical migration pattern being observed with equine RVA isolates with the segment 3 & 4 migrating together close to each other and unlike the other RVA isolates

here the segment 7, 8 and 9 migrate as a triplet (Hardy et al., 1991).

ELISA and other immunodiagnostic have been now used for rapid detection of RV which are usually based on the group specific VP6 gene product (outer coat protein). Many test kits available for human RV detection has also been employed in the detection of equine rotaviruses, though the sensitivity of ELISA has been found more in respect to other immunodiagnostic test (Nemoto et al., 2010a). The indication of widespread RVA infections in horses was evident by the finding of RVA specific antibodies in adult horses (Pearson et al., 1982; Eichhorn & Huan-Chun, 1987). It was also evident by the detection of RVA in equine population from different countries which includes the United Kingdom (Strickland et al., 1982), the United States of America (Kanitz, 1977), Australia (Studdert et al., 1978; Tzipori & Walker, 1978) Germany (Elschner et al., 2005), New Zealand (Durham et al., 1979; Schroeder et al., 1983), France (Puyalto-Moussu & Taouji, 2002), Greece (Ntafis et al., 2010), Italy (Monini et al., 2011), the Netherlands (Van der Heide et al., 2005), Argentina (Barrandeguy et al., 1998), Venezuela (Ciarlet et al., 1994) and India (Gulati et al., 2009).

RT-PCR assays are being used as test of choice nowadays for the detection as well as for genotyping of equine RVA strains (Gouvea et al., 1994; Tsunemitsu et al., 2001; Garaicoechea et al., 2011). Hybridizing probe based diagnostics and genotyping has also been attempted in bovine rotavirus which can be opted for equine strains too (Minakshi et al., 2005). More recently, one isothermal technique RT-LAMP has been developed targeting the VP4 with P[12] specificity (Nemoto et al., 2010b). Moreover, in USA RT-PCR kit is commercially available for early and quick detection of RVs (Slovic et al., 2010). As submissions of molecular sequence of rotavirus have been increased in public database, sequence based typing of rotavirus groups got interest. Till now, there have been 6 G-genotypes (Imagawa et al., 1994; Isa et al., 1994; Isa et al., 1996) and 6 P-genotypes (Garaicoechea et al., 2011) are reported in equines (Table 2).

Table 2 G and P genotypes of equines rotaviruses reported till date.

G-Type	P-Type
G3	P[1]
G5	P[3]
G8	P[7]
G10	P[11]
G13	P[12]
G14	P[18]

Among the widely reported and commonly found genotype combinations of equine RVA, G3P[12] and G14P[12] have been described several times worldwide (Tsunemitsu et al., 2001; Elschner et al., 2005; Collins et al., 2008; Ntafis et al., 2010; Garaicoechea et al., 2011; Nemoto et al., 2011 Papp et

al., 2013). The G3 RVA strains have been further differentiated into 2 subtypes (G3A and G3B) as per reactivity with monoclonal antibodies (Browning et al., 1992). In the year 1991, a highly unfamiliar equine RVA strain (L338) carrying G13P[18] genotype combination was reported from UK (Browning et al., 1991a). Using the RNA-RNA hybridization technique, it was shown that the strain L338 possess a distinctive genotype of G13 and P[18] and unusual NSP1 genetic makeup which found distinct to other human and animal RVAs (Wu et al., 1993; Taniguchi et al., 1994; Kojima et al., 1996). Certain bovine-like equine RVAs have also been reported which are highly similar to bovine RV strains employing labeled probes and RNA-RNA hybridization techniques from UK and Japan, respectively (Imagawa et al., 1991; Imagawa et al., 1993; Isa et al., 1996),

Similarly, an unusual G6 and G10P6[1] rotavirus was detected in equines between 2003 and 2005 in addition to G1 strains from India, but later this report was taken back following the wrong classification of G6 RVA strains as G16 (Matthijnsens et al., 2012b). In Argentina also an uncommon feline-like RVA was also reported in diarrheic foal (Garaicoechea et al., 2011). Certain unusual equine RVA genotype combinations has also been discovered such as G3P[3], G5P[7], G6P[1], G8P[1], G10P[1], G10P[11] and G13P[18], (Gulati et al., 2007; Garaicoechea et al., 2011). Till date only three inactivated equine RVA vaccine have developed by Argentina, Japan and USA and are being used in several countries contains the common genotype of G3P[12] strain (Imagawa et al., 2005).

During three decades (1981-2010) there have been several studies in Japan leading to the genetic analysis and characterization of equine RVAs (Takagi et al., 1994; Tsunemitsu et al., 2001; Fukai et al., 2006; Nemoto et al., 2012;). Till 2013 only few reports for the whole genome characterization and analysis of equine RVA strains have been documented (Ghosh et al., 2012; Matthijnsens et al., 2012b; Mino et al., 2013). The strains characterized for their complete genomic constellations were three from Europe (Strain: L338; 03V04954 and 04V2024), three from Argentina (Strain: E30; E403 and E4040), one from South Africa (Strain: EqRV-SA1) and four from Japan (Strain: B1; HH-22; CH-3 and OH-4) (Ghosh et al., 2012; Matthijnsens et al., 2012b; Ghosh et al., 2013; Mino et al., 2013).

In February 2015, a report appeared in which 23 equine RVA strains from late 1990s and 2009-2010 along with the vaccine strain HO-5 were characterized through the next generation sequencing (Nemoto et al., 2015c) taking the total count of whole genome reports for equine RVA to 37 isolates till dates (Table 2). In the whole genome and further phylogenetic analysis of 37 isolates revealed that the G3 strains carried a uniform genetic constellation for their 11 gene segments and were closely related to the HO-5 vaccine strain irrespective of time they were confirmed (Nemoto et al., 2015c). In disparity, the G14 strains showed some divergence in respect to VP7 and NSP4 gene.

Figure 1 Whole genome backbone consisting of 11 segments of equine group A rotavirus (RVA) strains with known genomic constellations.

SL. No	Strain Name	Year of Isolation	VP7	VP4	VP6	VP1	VP2	VP3	NSP1	NSP2	NSP3	NSP4	NSP5	Reference
1	RVA/Horse-wt/ARG/E403/2006/G14P[12]	2006	G14	P[12]	I2	R2	C2	M3	A10	N2	T3	E12	H7	Matthijnssens et al. (2012)
2	RVA/Horse-wt/ARG/E4040/2008/G14P[12]	2008	G14	P[12]	I2	R2	C2	M3	A10	N2	T3	E12	H7	Matthijnssens et al. (2012)
3	RVA/Horse-wt/ARG/E30/1993/G3P[12]	1993	G3	P[12]	I6	R2	C2	M3	A10	N2	T3	E12	H7	Matthijnssens et al. (2012)
4	RVA/Horse-wt/IRL/03V04954/2003/G3P[12]	2003	G3	P[12]	I6	R2	C2	M3	A10	N2	T3	E2	H7	Matthijnssens et al. (2012)
5	RVA/Horse-wt/IRL/04V2024/2004/G14P[12]	2004	G14	P[12]	I2	R2	C2	M3	A10	N2	T3	E2	H7	Matthijnssens et al. (2012)
6	RVA/Horse-wt/ZAF/EqRV-	2006	G14	P[12]	I2	R2	C2	M3	A10	N2	T3	E2	H7	Matthijnssens et al. (2012)
7	RVA/Horse-tc/GBR/L338/1991/G13P[18]	1991	G13	P[18]	I6	R9	C9	M6	A6	N9	T12	E14	H11	Matthijnssens et al. (2012)
8	RVA/Horse-wt/ARG/E3198/2008/G3P[3]	2008	G3	P[3]	I3	R3	C3	M3	A9	N3	T3	E3	H6	Mino et al. (2013)
9	RVA/Horse-tc/GBR/H-1/1975/G5P9[7]	1975	G5	P[7]	I5	R1	C1	M1	A8	N1	T1	E1	H1	Ghosh et al. (2013)
10	RVA/Horse -tc/JPN/OH -4/1982/G6P[5]	1982	G6	P[5]	I2	R2	C2	M2	A13	N2	T6	E2	H3	Ghosh et al. (2013)
11	RVA/Horse -tc/JPN/B1/1981/G3P[12]	1981	G3	P[12]	I2	R2	C2	M3	A10	N2	T3	E2	H7	Ghosh et al. (2013)
12	RVA/Horse -tc/JPN/HH -22/1989/G 3P[12]	1989	G3	P[12]	I6	R2	C2	M3	A10	N2	T3	E2	H7	Ghosh et al. (2013)
13	RVA/Horse -tc/JPN/CH -3/1987/G14P[12]	1987	G14	P[12]	I2	R2	C2	M3	A10	N2	T3	E2	H7	Ghosh et al. (2013)
14	RVA/Horse-tc/JPN/HO-5/1982/G3P[12]	1982	G3	P[12]	I2	R2	C2	M3	A10	N2	T3	E2	H7	Nemoto et al. (2015c)
15	RVA/Horse-tc/JPN/IE29/1997/G3P[12]	1997	G3	P[12]	I2	R2	C2	M3	A10	N2	T3	E2	H7	Nemoto et al. (2015c)
16	RVA/Horse-tc/JPN/IE75/1997/G3P[12]	1997	G3	P[12]	I2	R2	C2	M3	A10	N2	T3	E2	H7	Nemoto et al. (2015c)
17	RVA/Horse-tc/JPN/IE76/1996-1997/G3P[12]	1996	G3	P[12]	I2	R2	C2	M3	A10	N2	T3	E2	H7	Nemoto et al. (2015c)
18	RVA/Horse-tc/JPN/IE97/1996/G3P[12]	1996	G3	P[12]	I2	R2	C2	M3	A10	N2	T3	E2	H7	Nemoto et al. (2015c)
19	RVA/Horse-tc/JPN/IE102/1997/G3P[12]	1997	G3	P[12]	I2	R2	C2	M3	A10	N2	T3	E2	H7	Nemoto et al. (2015c)
20	RVA/Horse-tc/JPN/No.1/2010/G3P[12]	2010	G3	P[12]	I2	R2	C2	M3	A10	N2	T3	E2	H7	Nemoto et al. (2015c)
21	RVA/Horse-tc/JPN/No.2/2010/G3P[12]	2010	G3	P[12]	I2	R2	C2	M3	A10	N2	T3	E2	H7	Nemoto et al. (2015c)
22	RVA/Horse-tc/JPN/No.4/2010/G3P[12]	2010	G3	P[12]	I2	R2	C2	M3	A10	N2	T3	E2	H7	Nemoto et al. (2015c)
23	RVA/Horse-tc/JPN/No.7/2010/G3P[12]	2010	G3	P[12]	I2	R2	C2	M3	A10	N2	T3	E2	H7	Nemoto et al. (2015c)
24	RVA/Horse-tc/JPN/No.9/2010/G3P[12]	2010	G3	P[12]	I2	R2	C2	M3	A10	N2	T3	E2	H7	Nemoto et al. (2015c)
25	RVA/Horse-tc/JPN/No.13/2010/G3P[12]	2010	G3	P[12]	I2	R2	C2	M3	A10	N2	T3	E2	H7	Nemoto et al. (2015c)
26	RVA/Horse-tc/JPN/No.32/2010/G3P[12]	2010	G3	P[12]	I2	R2	C2	M3	A10	N2	T3	E2	H7	Nemoto et al. (2015c)
27	RVA/Horse-tc/JPN/No.52/2009/G3P[12]	2009	G3	P[12]	I2	R2	C2	M3	A10	N2	T3	E2	H7	Nemoto et al. (2015c)
28	RVA/Horse-tc/JPN/No.55/2009/G3P[12]	2009	G3	P[12]	I2	R2	C2	M3	A10	N2	T3	E2	H7	Nemoto et al. (2015c)
29	RVA/Horse-tc/JPN/IE77/1997/G14P[12]	1997	G14	P[12]	I2	R2	C2	M3	A10	N2	T3	E2	H7	Nemoto et al. (2015c)
30	RVA/Horse-tc/JPN/IE81/1997/G14P[12]	1997	G14	P[12]	I2	R2	C2	M3	A10	N2	T3	E2	H7	Nemoto et al. (2015c)
31	RVA/Horse-tc/JPN/IE84/1996/G14P[12]	1996	G14	P[12]	I2	R2	C2	M3	A10	N2	T3	E2	H7	Nemoto et al. (2015c)
32	RVA/Horse-tc/JPN/IE87/1996-1997/G14P[12]	1996	G14	P[12]	I2	R2	C2	M3	A10	N2	T3	E2	H7	Nemoto et al. (2015c)
33	RVA/Horse-tc/JPN/IE115/1997/G14P[12]	1997	G14	P[12]	I2	R2	C2	M3	A10	N2	T3	E2	H7	Nemoto et al. (2015c)
34	RVA/Horse-tc/JPN/No.24/2010/G14P[12]	2010	G14	P[12]	I2	R2	C2	M3	A10	N2	T3	E2	H7	Nemoto et al. (2015c)
35	RVA/Horse-tc/JPN/No.28/2010/G14P[12]	2010	G14	P[12]	I2	R2	C2	M3	A10	N2	T3	E2	H7	Nemoto et al. (2015)
36	RVA/Horse-tc/JPN/No.29/2010/G14P[12]	2010	G14	P[12]	I2	R2	C2	M3	A10	N2	T3	E2	H7	Nemoto et al. (2015c)
37	RVA/Horse-tc/JPN/No.50/2010/G14P[12]	2010	G14	P[12]	I2	R2	C2	M3	A10	N2	T3	E2	H7	Nemoto et al. (2015c)

The NSP4 gene of G14 strains and also G3 strains clustered along with bovine RVAs and bovine-like equine strain OH-4 and HH-22, whereas rest all other genes were identical to HO-5 vaccine strain (Nemoto et al., 2015c). The common backbone of the equine RVAs has been shown in Table 2 comprising all the whole genome isolates.

Almost all the common whole genome equine RVA strains characterized previously showed conserved genotypic constellation among them and were divergent in nature to the other RVA isolates (Matthijnssens et al., 2012b). Whereas few equine RVA strains characterized showed unique genetic makeup and elaborated the possibility of interspecies jumping of RVAs from one species to the other (Figure 1). The strains showing the possibility of interspecies transmission were equine G3P[18] RVA strain L338 (Matthijnssens et al., 2012b), H-1 strain believed to be transmitted from pigs to equines (Ghosh et al., 2012), whereas strain E3198 seemed to be resultant of canine/feline RVA strain to equines (Mino et al., 2013). Further, strengthening the need to analyze more common and uncommon equine RVA strains around the world the analysis done by two research groups were remarkable (Matthijnssens et al., 2012b; Ghosh et al., 2013). These reports established the fact that more or less out of the 11 segments of RVAs the interspecies transmission event are constantly changing the nature of equine RVA being detected in the horse population worldwide. While a report from UK reported that the strain L338 has no closeness with any other rotavirus and thus confirms that few strains remains solely adaptable to equine with no sign of interspecies transmission (Ciarlet et al., 2001).

Although out of the eleven segments of RVA, eight showed the conserved nature among the equine RVAs, whereas only VP6, VP7 and NSP4 genes showed existence of 2 diverse genotypes: I2/I6, G3/G14 and E2/E12, respectively. These reports also hypothesized the presence of distinguished lineages present among the common equine genotype constellations. At least three lineages of equine genomic constellation are circulating among equine rotaviruses since 1990s including G3-P[12]-I6-E2 lineage I, G14-P[12]-I2-E2 lineage I, and G14-P[12]-I2-E2 lineage II (Nemoto et al., 2015c). Though these lineages are interim therefore more complete information will be needed to decipher the relationship of these lineages. Unusually the three complete genome reports of equine RVA from Argentina showed the presence of E12 NSP4 genotype which were recently recovered from guanacos and the unusual bovine RVA strain (G15P[11]) from Argentina (Matthijnssens et al., 2009).

Further, this E12 genotype was also detected in all analyzed isolates from 1998 to 2008 in Argentinian foals (Garaicoechea et al., 2011). Certain unpublished data also shown the incidence of E12 NSP4 genotype in Argentinean goat and cattle population. But it was surprising to find that NSP4 E12 genotype is only confined to equine RVA strains to much of extent which may be the success indicator of quarantine procedures involved in the transportation of horses which

restricted its transmission to other continents. But no such geographical barrier is present between the African and European equine RVA strains as two strains (04V2024 and EqRV-SA1) shared nearly identical genotype G14P[12] identified in South Africa and Ireland, respectively.

Presence of bovine RVA like NSP4 gene in conserved equine backbone from Japan points towards the probability of equine rotavirus as an acceptor of gene segments from different host species and vice-versa (Nemoto et al., 2015b). Detection of equine origin G3 genotype of VP7 in humans from Asia, Australia and Europe confirms the possible host species jump event of equine rotavirus to human hosts (Malasao et al., 2015; Cowley et al., 2016). Lately, similar reports emerged from Spain and Hungary concerning the emergence of unusual G3P[8] type rotaviruses in humans wherein the VP7 gene represents an equine like G3 (Arana et al., 2016; Dóro et al., 2016). These evolutionary phenomenon i.e. reassortment and species jumping leads to rotavirus genetic diversity which eventually pose a threat to human and other animal host species. Therefore, a more rigorous surveillance programs are prerequisite to establish geographical relationship among the equine rotavirus strains.

5 Picobirnavirus

Picobirnaviruses (PBVs) are small, un-enveloped viruses containing bi-segmented dsRNA genome. They contains ~2.5 kbp segments 1 and ~1.7 kbp for the segment 2 (Malik et al., 2014). The segment I encodes for the single structural capsid protein gene and segment 2 encodes the viral RNA polymerase (RdRp). It is placed in a new viral family namely *Picobirnaviridae* and is assigned a new taxonomic order which contains a single genus *Picobirnavirus*. The genus include only two species i.e. Human *Picobirnavirus* and Rabbit *Picobirnavirus* (Malik et al., 2014). The human PBV serves as the type species whereas the rabbit PBV serves as the designated species according to the ICTV. Based on the RdRp gene segment 2, PBVs are grouped into 2 genogroups (genogroup-I and II). Recent studies also proposed possible new genogroup namely III, IV and V based on the diversity of RdRp sequences (Smits et al., 2014; Li et al., 2015). The proposed new groups include strains from human (group III and V), dromedary (group V) and equine (group IV and V). Equine PBV strains have been identified in horse blood plasma (Li et al., 2015).

With the advancement of molecular diagnostic techniques such as RT-PCR (Ganesh et al., 2012; Malik et al., 2013; Takiuchi et al., 2016) and qRT-PCR (Malik, unpublished data) for picobirnaviruses, they have been detected in faecal and respiratory samples from over 20 animal species including rodents, aves and large animals like rats, hamsters, guinea pigs, giant ant eater, dogs, pigs, bovine calves, buffalo calves, foals camels, snakes worldwide and exhibit vast genetic diversity (Ganesh et al., 2011; Malik et al., 2011; Smits et al., 2011; Gillman et al., 2013; Malik et al., 2013; Malik et al., 2014; Ng et al., 2014; Ribeiro et al., 2014; Woo et al., 2014, Verma et

al., 2015; Takiuchi et al., 2016). Despite the broad host range, pathogenicity of PBVs alone or as co-infecting agents remains unclear.

In equines, PBVs have been reported for the first time in the year 1991 in foals in Ireland and Britain (Browning et al., 1991b), followed by the RT-PCR detection in a female foal from Kolkata, India (Ganesh et al., 2011). Recently, equine PBVs co-infections were detected in plasma of a horse showing depression, loss of appetite (Li et al., 2015). Sequence analysis of viral RdRp and capsid genes showed four highly diverse picobirnaviruses including a novel fused picobirnavirus genome. These few reports of equine PBVs deserves attention regarding their epidemiological study and towards the development of diagnostic tools.

6 Miscellaneous Enteric Viral Infections

Several other viruses have also been shown to induce diarrhea like symptoms in neonatal or young foals but their relevance to enteritis less studied. Parvovirus in animals is usually known for its diarrheal symptoms but in equines it is reported in aborted equine fetus (Wong et al., 1985). Of late, parvovirus was recorded in cerebrospinal fluid (CSF) of a horse exhibiting neurological signs (Li et al., 2015). The study also enlist some other enteric viruses with no relevance to enteritis in equine namely anelloviruses, cyclovirus, kirkovirus etc. The scanty data on these viruses especially in equines is still lacking.

Conclusion

Many diseases have their multifactorial causes with different symptoms and etiologies. A peculiar type of immune response is prompted by a particular pathogen whereas, other co-infecting pathogens make it complex. In veterinary medicine, the documentation of GIT infections with co-infecting pathogens has not been well studied. Especially in equines, the knowledge of co-infections is very scarce. Different enteric viruses have different symptoms and their spread can be controlled by better diagnosis and intensive care of the foals. Prognosis for a young foal with diarrhea varies according to the causative virus and hence the severity of clinical signs also changes.

Apart from vaccine development other options such as herbal preparations can be also tried as potential preventive alternative. Since enteric infections are a big challenge worldwide we need to explore better preventive options available as anything might prove efficient and miraculous in preventing these infection in days to come. For inactivation of the environmental contamination through virus shedding, proper disinfectants must be opted as well as selection of better hand sanitizers must be taken care. Therefore, better management practices, nutritional management, diagnosis and treatment strategy according to the causative virus is important for the equine health.

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Conflict of interest

Authors would hereby like to declare that there is no conflict of interests that could possibly arise.

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